

FIGURE 1

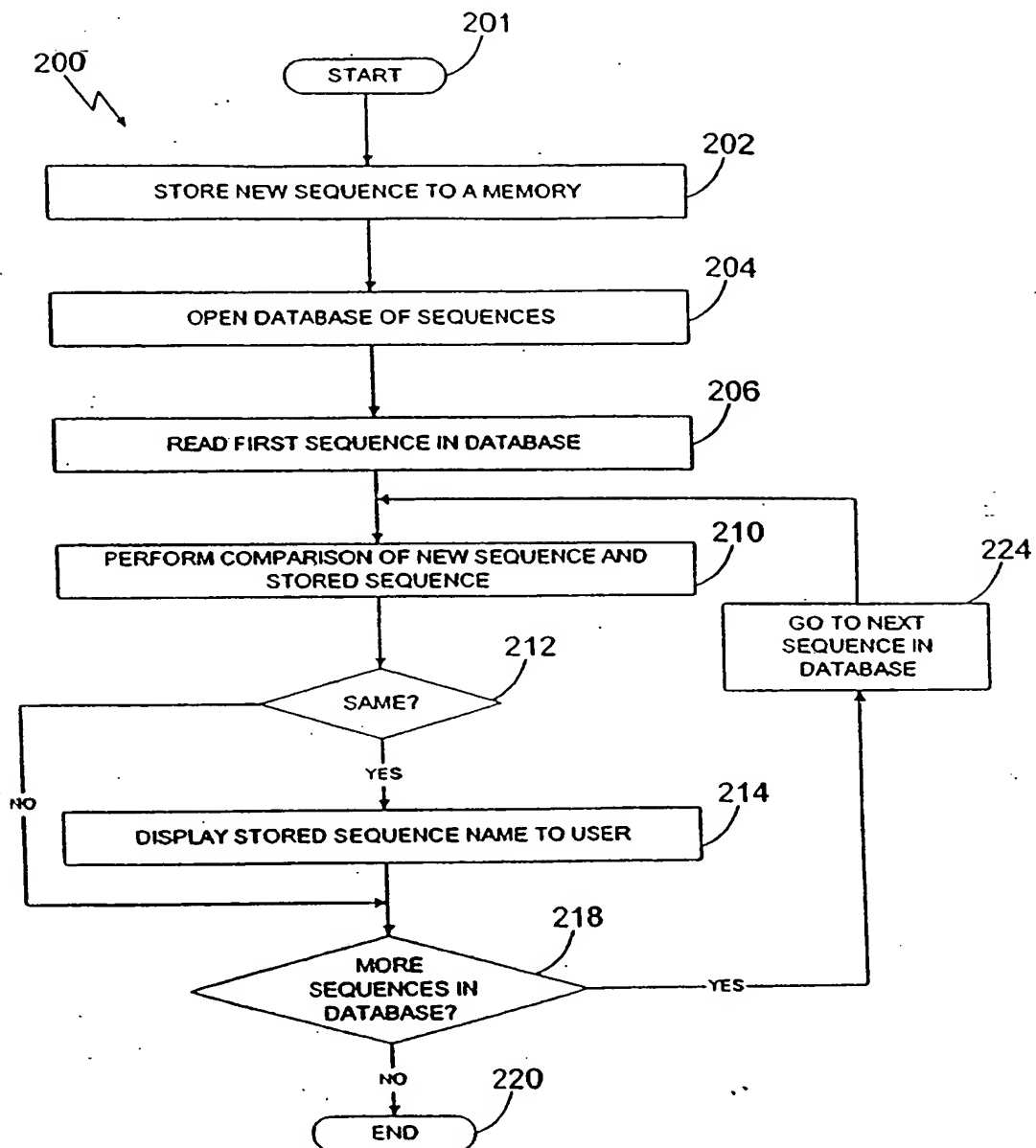


FIGURE 2

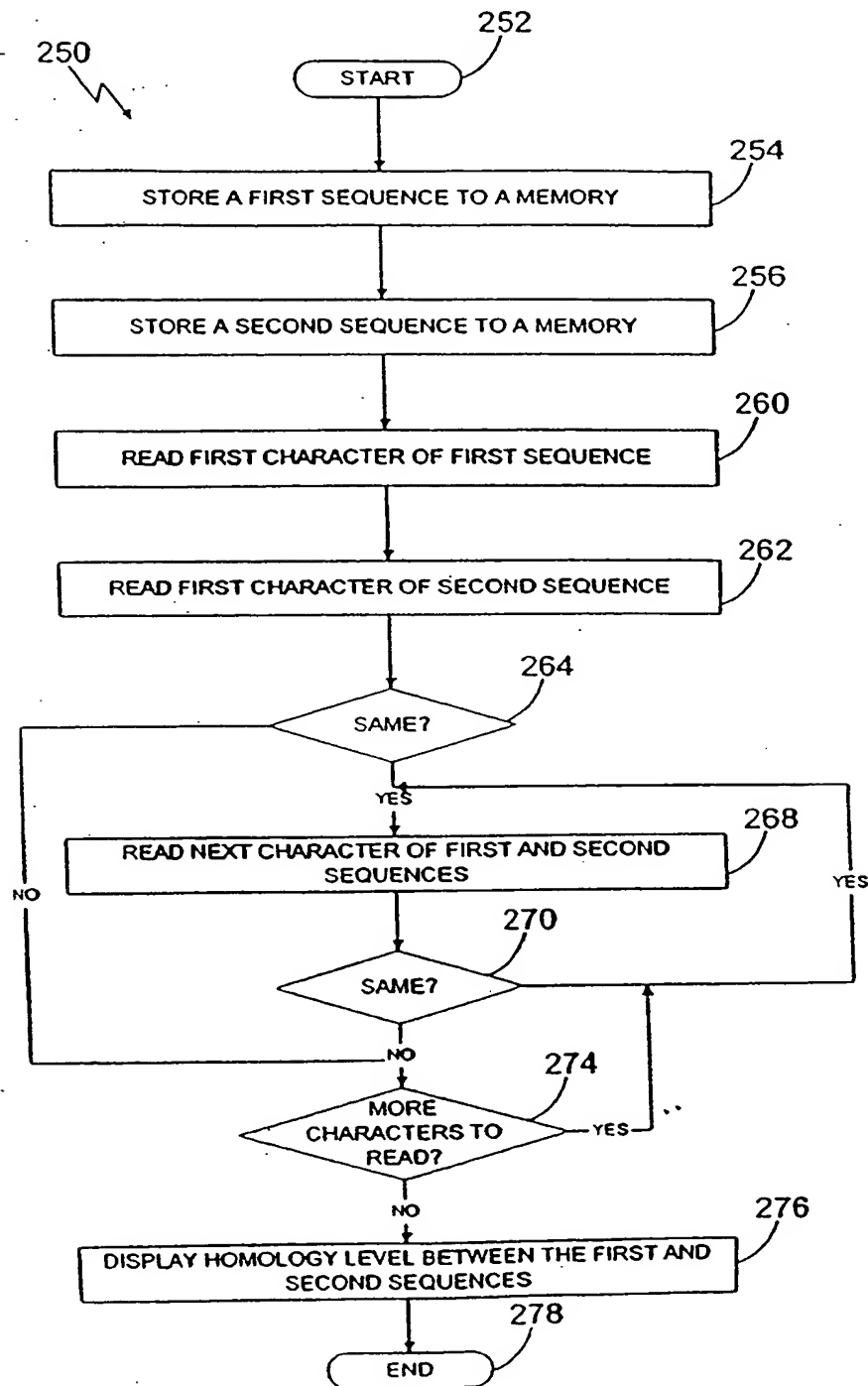


FIGURE 3

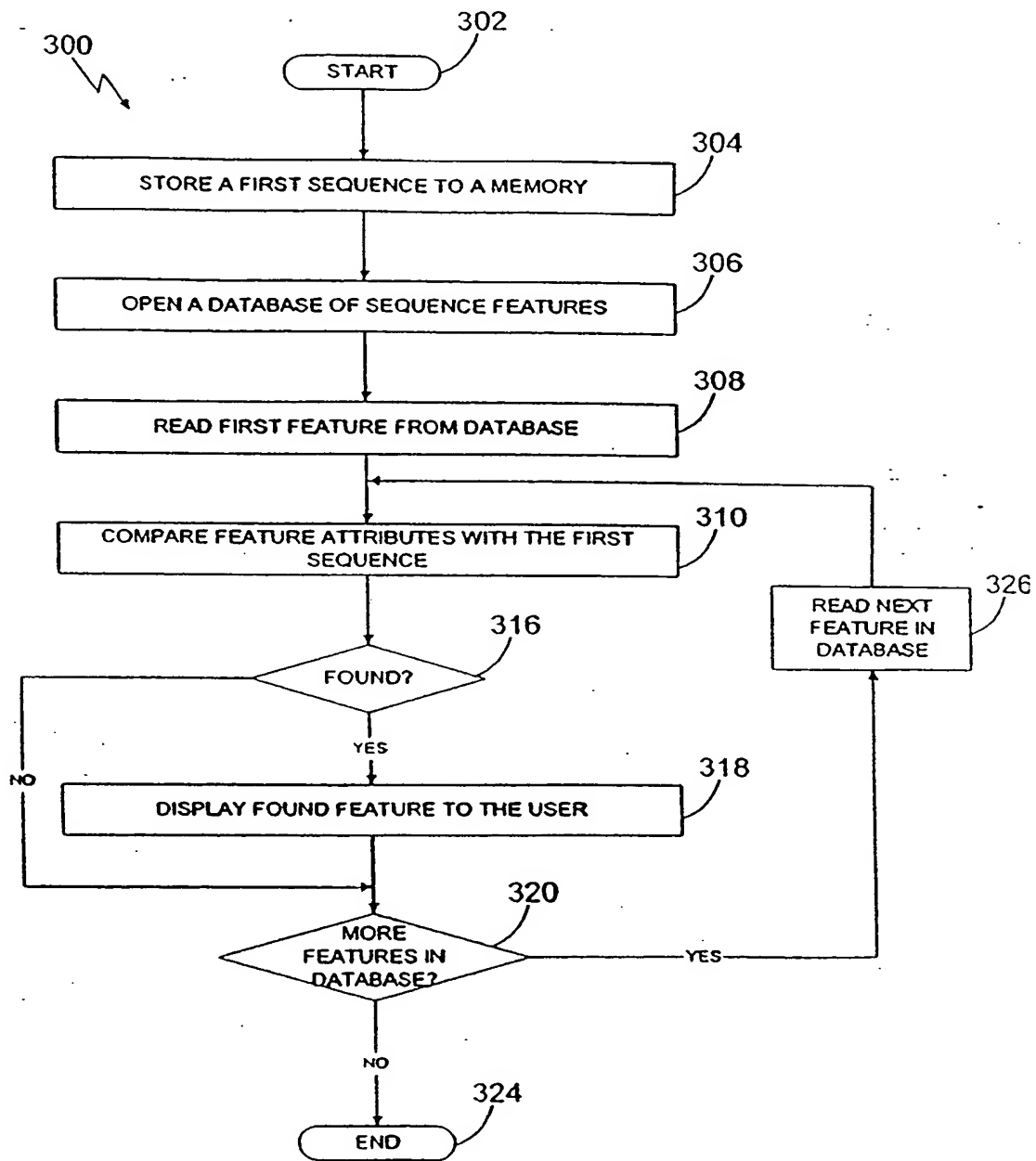


FIGURE 4

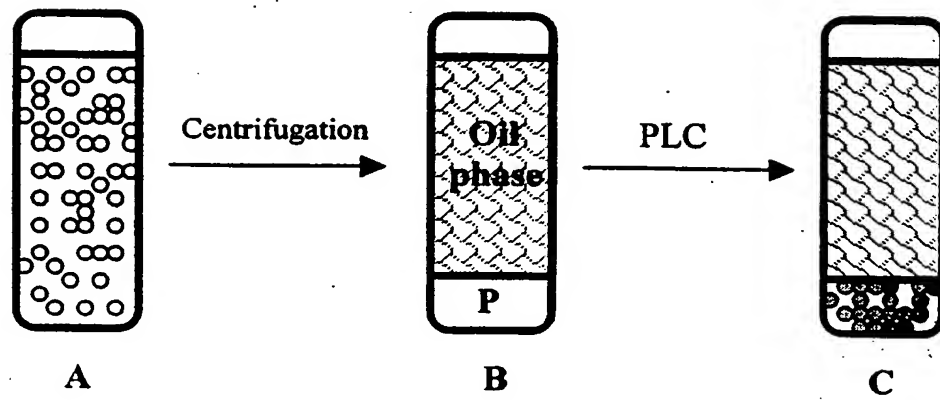


FIGURE 5

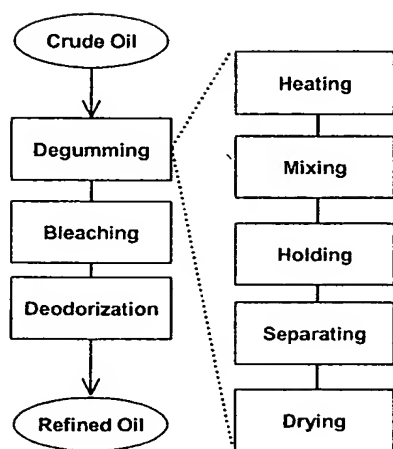


FIGURE 6

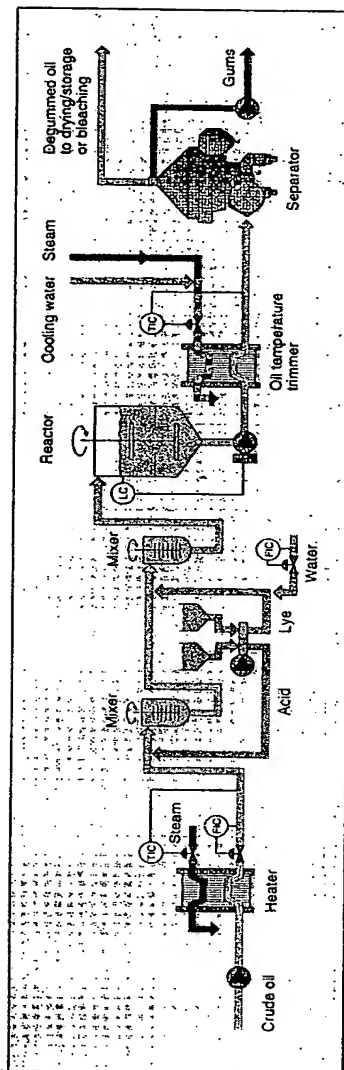


FIGURE 7

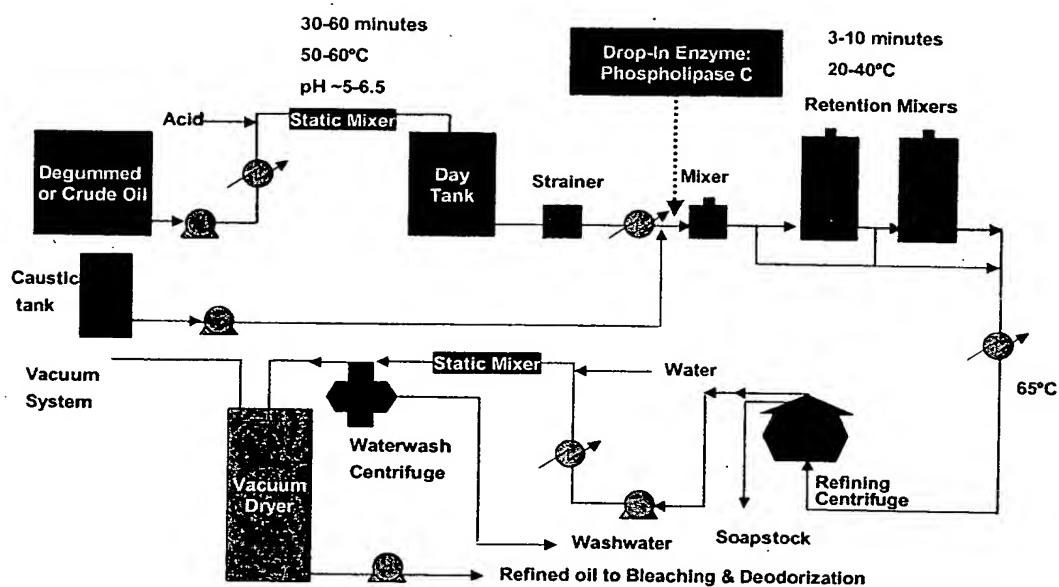


FIGURE 9

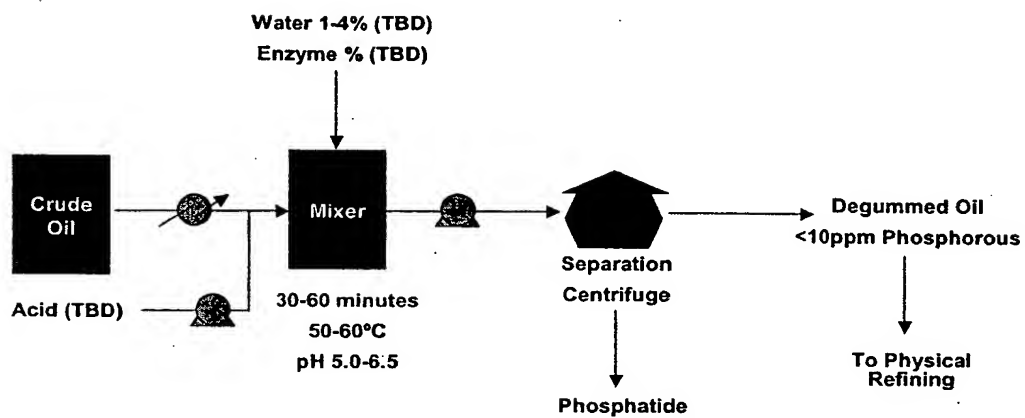


FIGURE 10

1,2	gij2815227 emb CAA76148.1	e-94	Phosphatidyl- degrading phospholipase C	Bacillus thuringiensis	N/A	80.5	79.3	287	283
3,4	gij2815227 emb CAA76148.1	e-94	Phosphatidyl- degrading phospholipase C	Bacillus thuringiensis	N/A	77.3	77	283	283
5,6	gij130081 spP09 598	e-134	Phosphatidyl- degrading phospholipase C	Bacillus cereus	N/A	77	76	280	272
7,8	gij3044072 gb AAC13276.1	e-97	Beta-hemolysin	Staphylococcus schleiferi	N/A	54	33	330	329

FIGURE 11A

PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM
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9, 10	beta-hemolysin - Staphylococcus aureus	Staphylococcus aureus	3.1.4.3	97788	9E-34	14647263	999	332	993	331	32
11, 12			3.4.21.-	23474722	3E-52	14278066	1041	346	N/A	339	38
13, 14			3.4.21.-	23474722	7E-55	14530226	1038	345	N/A	339	38
15, 16	hypothetical protein [Pseudomonas aeruginosa PA01]	Pseudomonas aeruginosa PA01		15598123	1E-102	9949021	1344	447	1329	443	46
17, 18			3.1.1.4	23127917	4E-24	14670061	1137	378	N/A	391	29
19, 20				27367835	0	3748408	1248	415	N/A	417	72
21, 22	phospholipase C [Aeromonas hydrophila]	Aeromonas hydrophila		3746953	1E-169	3746952	1716	571	1716	572	53
23, 24	conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913]			21232725	2E-51	4753846	1473	490	1344	448	31
25, 26			3.4.21.-	23474722	4E-50	13938818	1098	365	N/A	339	36
27, 28				23474722	4E-26	13173617	1287	428	N/A	339	27
29, 30	conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913]			21233052	0.00007	14589793	753	250	1311	437	20
31, 32	phospholipase C (EC 3.1.4.3) precursor - Bacillus cereus	Bacillus cereus	3.1.4.3	2126777	2E-48	11558558	1422	473	1776	592	32
33, 34	hypothetical protein [Xanthomonas campestris]	Xanthomonas campestris		6689533	1E-18	1180468	792	263	855	285	30
35, 36	Sequence 2 from patent US 5824864			5972806	5E-14	2723462	1389	462	1230	410	20
37, 38	phospholipase C [Aeromonas hydrophila]	Aeromonas hydrophila		3746953	1E-149	3746952	1329	443	1716	572	59
39, 40	hypothetical protein [Pseudomonas aeruginosa PA01]	Pseudomonas aeruginosa PA01		15598123	1E-106	9949021	1335	444	1329	443	49
41, 42	conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306]	Xanthomonas axonopodis pv. citri str. 306		21241345	2E-63	3885908	1419	472	1320	440	35
43, 44				23474722	4E-26	13529454	1287	428	N/A	339	27
45, 46			3.4.21.-	23474722	4E-55	14530226	1038	345	N/A	339	38
47, 48	hypothetical protein [Nostoc sp. PCC 7120]	Nostoc sp. PCC 7120		17230632	6E-25	6322016	1476	491	1365	455	23
49, 50				27367835	1E-166	10898526	1257	418	N/A	417	65
51, 52	conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913]			21232725	2E-50	13122711	1482	493	1344	448	30
53, 54	hypothetical protein [Pseudomonas aeruginosa PA01]	Pseudomonas aeruginosa PA01		15598123	1E-16	13928640	1491	496	1329	443	22
55, 56			3.4.21.-	23474722	2E-53	8896126	1041	346	N/A	339	39
57, 58	hypothetical protein [Pseudomonas aeruginosa PA01]	Pseudomonas aeruginosa PA01		15598123	1E-18	3337392	1413	470	1329	443	22
59, 60			3.4.21.-	23474722	9E-66	14280415	1038	345	N/A	339	39
61, 62	lecithinase [Vibrio mimicus]			3748409	0	3748408	1257	418	1410	470	77
63, 64				27367835	1E-173	3748408	1242	413	N/A	417	87
65, 66			3.1.1.4	23041851	3E-19	14993667	1164	387	N/A	337	32
67, 68	hypothetical protein [Pseudomonas aeruginosa PA01]	Pseudomonas aeruginosa PA01		15598123	9E-25	13880526	1419	472	1329	443	26
69, 70			3.4.21.-	23474722	9E-58	14530226	1038	345	N/A	339	38

FIGURE 11B

PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM
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71, 72	chitinase (EC 3.2.1.14) A - Pseudoalteromonas sp. (strain S9)	Pseudoalteromonas sp.	3.2.1.14	7521919	2E-28	7340814	3284	1088	3182	1054	11
73, 74	conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913]			21233052	0.00007	14589783	753	250	1311	437	20
75, 76	hypothetical protein [Pseudomonas aeruginosa PA01]	Pseudomonas aeruginosa PA01		15598123	1E-22	13157820	1335	444	1329	443	21
77, 78			3.4.21.-	23474722	4E-52	14550312	1028	341	N/A	339	36
79, 80	phospholipase C [Aeromonas hydrophila]	Aeromonas hydrophila		3746853	1E-188	15022388	1701	568	1716	572	52
81, 82	PHOSPHOLIPASE C PRECURSOR (PLC) (PHOSPHATIDYLCHOLINE PHOSPHOHYDROLASE) (CEREOLYSIN A)	Bacillus cereus	3.1.4.3	130081	1E-49	8570206	1422	473	849	283	26
83, 84	hemolysin [Vibrio parvulus]	Vibrio parvulus		10998525	5E-61	10716598	1290	429	1254	418	33
85, 86			3.4.21.-	23474722	1E-55	14530228	1038	345	N/A	339	38
87, 88			3.4.21.-	23041851	3E-12	11121040	870	289	N/A	337	28
89, 90	PHOSPHOLIPASE C PRECURSOR (PLC) (PHOSPHATIDYLCHOLINE PHOSPHOHYDROLASE) (CEREOLYSIN A)	Bacillus cereus	3.1.4.3	130081	1E-49	8570206	1422	473	849	283	26
91, 92			3.4.21.-	23474722	4E-54	3947685	1035	344	N/A	339	38
93, 94	beta-hemolysin - Staphylococcus aureus	Staphylococcus aureus	3.1.4.3	97788	6E-85	3044071	863	320	993	331	54
95, 96			3.4.21.-	23474722	2E-52	13518253	1038	345	N/A	339	38
97, 98	phospholipase C (EC 3.1.4.3) precursor - Bacillus cereus	Bacillus cereus	3.1.4.3	2126777	2E-49	3766134	1422	473	1778	592	32
99, 100			3.1.4.3	23129073	4E-43	7544033	1053	350	N/A	698	34
101, 102			3.1.4.3	27466928	3E-73	5802872	998	331	N/A	334	45
103, 104	Y4II [Rhizobium sp. NGR234]	Rhizobium sp. NGR234		16519782	3E-07	6755291	2205	734	2109	703	15
105, 106	Phospholipase C related protein [Clostridium acetobutylicum]	Clostridium acetobutylicum		15894308	0.005	2182412	758	251	735	245	18

FIGURE 11C

SEQ ID NO	NR Description	Accession	NR E-value	NR Organism	Gene seq Protein Description	Gene seq Protein Accession	Gene seq Protein E-value	Gene seq DNA Description	Gene seq DNA Accession	Gene seq DNA E-value	Pre-dicted EC No.	Query DNA Length	Query Protein Length	seq or NR DNA Length	seq or NR Protein Length	Gene seq or NR %ID	Gene seq or NR Protein %ID
107, 108	1-phosphatidylinositol phosphodiesterase precursor or [Bacillus cereus ATCC 14579]	30021854	0	Bacillus cereus ATCC 14579	Listeria monocytogenes protein #849	ABB47680	3E-18	Arabidopsis yellow stripe1-like 4 SEQ ID NO 10	ABN85766	0.25	3.1.4.10	990	329	990	329	92	91
109, 110	1-phosphatidylinositol phosphodiesterase precursor or [Bacillus cereus ATCC 14579]	30021854	0	Bacillus cereus ATCC 14579	Listeria monocytogenes protein #849	ABB47680	6E-18	Arabidopsis yellow stripe1-like 4 SEQ ID NO 10	ABN85766	0.25	3.1.4.10	990	329	990	329	92	92

FIGURE 11D

111, 112	phosphatidylinositol-specific phospholipase C [Listeria seeligeri]	2231002	8E-25	Listeria seeligeri	Listeria monocytogenes protein #849	ABB47680	2E-24	RCC	ABX74467	3.2	3.1.4.10	828	275	963	320	31	42
113, 114	1-phosphatidylinositol phosphodiesterase precursor or [Bacillus cereus ATCC 14579]	30021854	1E-180	Bacillus cereus ATCC 14579	Listeria monocytogenes protein #849	ABB47680	8E-18	Arabidopsis yellow stripe 1-like 4 SEQ ID NO 10	ABN85766	0.24	3.1.4.10	981	326	990	329	92	92
115, 116	1-phosphatidylinositol phosphodiesterase precursor or [Bacillus cereus ATCC 14579]	30021854	1E-178	Bacillus cereus ATCC 14579	Listeria monocytogenes protein #849	ABB47680	2E-16	Murine apoptosis related DNA sequence #201	ABL01358	0.97	3.1.4.10	987	328	990	329	89	90

FIGURE 11E

117, 118	1-phosphatidylinositol phosphodiesterase precursor or [Bacillus cereus ATCC 14579]	30021854	1E-179	Bacillus cereus ATCC 14579	Listeria monocytogenes protein #849	ABB47680	8E-16	ABZ57017	0.97	3.1.4.10	987	328	990	329	90	91
								Human central cannabinoid receptor 47.08 probe, SEQ ID NO:9								
119, 120	1-phosphatidylinositol phosphodiesterase precursor or [Bacillus cereus ATCC 14579]	30021854	1E-178	Bacillus cereus ATCC 14579	Listeria monocytogenes protein #849	ABB47680	8E-16	Murthe apoptosis related DNA sequence #201	0.97	3.1.4.10	987	328	990	329	89	90

FIGURE 11F

121, 122	1-phosphatidylinositol phosphodiesterase precursor [Bacillus cereus ATCC 14579]	30021854	0	Bacillus cereus ATCC 14579	Listeria monocytogenes protein #849	ABB47680	3E-17	Arabidopsis yellow stripe1-like 4 SEQ ID NO 10	ABN85766	0.016	3.1.4.10	990	329	990	329	92	92
123, 124	Phospholipase C [Bacillus cereus ATCC 14579]	30018852	1E-137	Bacillus cereus ATCC 14579	Listeria monocytogenes protein #849	ABB47676	1E-49	Human prostate cancer associated antigen nucleotide sequence SEQ ID:505	AAF22890	0.053	3.1.4.3	849	282	849	283	81	
125, 126	Y4II [Rhizobium sp. NGR234]	16519782	1E-69	Rhizobium sp. NGR234	DNA encoding novel human diagnostic protein #20574	ABG07933	0.045	M. capsulatus gene #766 for DNA array	ABQ91418	0.43		1710	569	2112	703	34	54

FIGURE 11G

conserved hypothetical protein [Porphyromonas gingivalis W83] 127, 128	34541487	2E-96	Porphyromonas gingivalis W83	Mycobacterium tuberculosis protein 10.	AB104710	2E-14	Human NS cDNA sequence SEQ ID	ABL39805	1	3.4.21.	1038	345	339	52
phospholipase C (EC 3.1.4.3) precursor - Bacillus cereus. 129, 130	2126777	2E-50	Bacillus cereus	Listeria monocytogenes protein #849.	ABB47676	2E-34	Human secretory polynucleotide SPTM SEQ ID	ABZ35958	0.36	3.1.4.3	1434	477	592	31
latex allergen from Hevea brasiliensis [Chromobacterium violaceum 131, 132]	34495896	4E-51	Chromobacterium violaceum ATCC 12472	Arabidopsis thaliana protein fragment SEQ ID NO:	AAG42787	4E-22	Arabidopsis thaliana protein fragment SEQ ID NO:	AAC42405	0.058	3.1.1.4	927	308	322	37

FIGURE 11H

133, 134	conserved hypothetical protein [Porphyromonas gingivalis W83]	34541487	1E-90	Porphyromonas gingivalis W83	10. ABJ04710	2E-20			3.4.21.	1053	350	2112	703	339	50	
135, 136	Y4II [Rhizobium sp. NGR234]	16519782	1E-69	Rhizobium sp. NGR234	DNA encoding novel human diagnostic protein #20574. ABG07933	1.5	Staphylococcus aureus DNA for cellular proliferation protein #1219. AAS51470	1.7		1710	569	2112	703	339	33	54
137, 138	conserved hypothetical protein [Porphyromonas gingivalis W83]	34541487	7E-97	Porphyromonas gingivalis W83	Mycobacterium tuberculosis protein 10. ABJ04710	2E-13	Human NS cDNA sequence ID NO:76. ABL39805	1	3.4.21.	1038	345			339	53	

FIGURE 11I

139, hydrophilic	phospholipase C [Aeromonas hydrophila]	3746953	1E-180	Aeromonas hydrophila	PCR primer for Topoisomerase II binding protein coding sequence	AAY03183	3.2	Angiotensin gene methylation analysis oligonucleotide #2	AAD28391	6.6	1692	563	1719	572	53	58
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FIGURE 11J

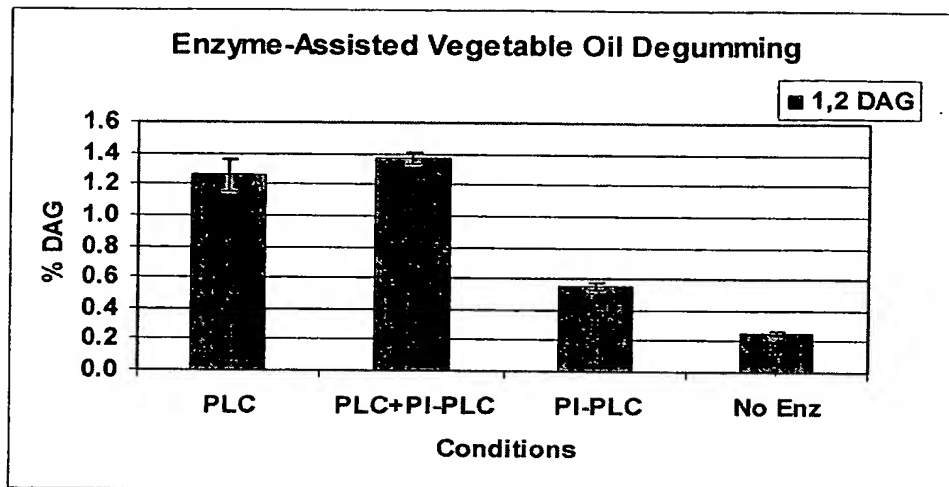


FIGURE 12